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1205

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## RAW SEQUENCE LISTING

DATE: 01/16/2002

PATENT APPLICATION: US/09/903,068

TIME: 15:53:53

Input Set : N:\Crf3\RULE60\09903068.raw

Output Set: N:\CRF3\01162002\I903068.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;  
6 Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik  
8 (ii) TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins  
9 Having Serine Threonine Kinase Domains And Their Use

11 (iii) NUMBER OF SEQUENCES: 29

13 (iv) CORRESPONDENCE ADDRESS:

- 14 (A) ADDRESSEE: Felfe & Lynch  
15 (B) STREET: 805 Third Avenue  
16 (C) CITY: New York City  
17 (D) STATE: New York  
18 (F) ZIP: 10022

20 (v) COMPUTER READABLE FORM:

- 21 (A) MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
22 (B) COMPUTER: IBM  
23 (C) OPERATING SYSTEM: PC-DOS  
24 (D) SOFTWARE: Wordperfect

26 (vi) CURRENT APPLICATION DATA:

- C--> 27 (A) APPLICATION NUMBER: US/09/903,068  
C--> 28 (B) FILING DATE: 11-Jul-2001

62 (vii) PRIOR APPLICATION DATA:

- 31 (A) APPLICATION NUMBER: 09/679,187  
32 (B) FILING DATE:  
35 (A) APPLICATION NUMBER: PCT/GB93/02367  
36 (B) FILING DATE: 17-November-1993  
39 (A) APPLICATION NUMBER: 9224057.1  
40 (B) FILING DATE: 17-November-1992  
43 (A) APPLICATION NUMBER: 9304677.9  
44 (B) FILING DATE: 8-March-1993  
47 (A) APPLICATION NUMBER: 9304680.3  
48 (B) FILING DATE: 8-March-1993  
51 (A) APPLICATION NUMBER: 9311047.6  
52 (B) FILING DATE: 28-May-1993  
55 (A) APPLICATION NUMBER: 9313763.6  
56 (B) FILING DATE: 2-July-1993  
59 (A) APPLICATION NUMBER: 9136099.2  
60 (B) FILING DATE: 3-August-1993  
63 (A) APPLICATION NUMBER: 9321344.5  
64 (B) FILING DATE: 15-October-1993

66 (viii) ATTORNEY/AGENT INFORMATION:

- 67 (A) NAME: Kohlei, Vineet  
68 (B) REGISTRATION NUMBER: 37,003

ENTERED

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69          (C) REFERENCE/DOCKET NUMBER: LUD 5298
71      (ix) TELECOMMUNICATION INFORMATION:
72          (A) TELEPHONE: (212) 688-9200
73          (B) TELEFAX: (212) 838-3884
77      (2) INFORMATION FOR SEQ ID NO: 1:
78          (i) SEQUENCE CHARACTERISTICS:
79              (A) LENGTH: 1984 base pairs
80              (B) TYPE: nucleic acid
81              (C) STRANDEDNESS: unknown
82              (D) TOPOLOGY: linear
83          (ii) MOLECULE TYPE: cDNA
84          (iii) HYPOTHETICAL: NO
85          (iv) ANTI-SENSE: NO
86          (v) FRAGMENT TYPE: internal
87          (vi) ORIGINAL SOURCE:
88              (A) ORGANISM: Homo sapiens
89      (ix) FEATURE:
90          (A) NAME/KEY: CDS
91          (B) LOCATION: 283..1791
92      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
94      AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA      60
96      AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC      120
98      GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCGCCGT      180
100     CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA      240
102     AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC      294
103                                     Met Thr Leu Gly
104                                     1
106     TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC TTG GTG ACC CAG      342
107     Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln
108         5              10              15              20
110     GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG ACC TGC ACG TGT      390
111     Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys Thr Cys
112         25              30              35
114     GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG GCC TGG TGC ACA      438
115     Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp Cys Thr
116         40              45              50
118     GTA GTG CTG GTG CGG GAG GAG GGG AGG CAC CCC CAG GAA CAT CGG GGC      486
119     Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His Arg Gly
120         55              60              65
122     TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC CCC ACC GAG TTC      534
123     Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr Glu Phe
124         70              75              80
126     GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC CAC AAC GTG TCC      582
127     Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn Val Ser
128     85              90              95              100
130     CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG CCG GGA ACA GAT      630
131     Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln Pro Gly Thr Asp
132         105              110              115
134     GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC TTG CTG GCC CTG      678

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135	Gly	Gln	Leu	Ala	Leu	Ile	Leu	Gly	Pro	Val	Leu	Ala	Leu	Leu	Ala	Leu	
136				120					125					130			
138	GTG	GCC	CTG	GGT	GTC	CTG	GGC	CTG	TGG	CAT	GTC	CGA	CGG	AGG	CAG	GAG	726
139	Val	Ala	Leu	Gly	Val	Leu	Gly	Leu	Trp	His	Val	Arg	Arg	Arg	Gln	Glu	
140			135					140					145				
142	AAG	CAG	CGT	GGC	CTG	CAC	AGC	GAG	CTG	GGA	GAG	TCC	AGT	CTC	ATC	CTG	774
143	Lys	Gln	Arg	Gly	Leu	His	Ser	Glu	Leu	Gly	Glu	Ser	Ser	Leu	Ile	Leu	
144		150					155					160					
146	AAA	GCA	TCT	GAG	CAG	GGC	GAC	ACG	ATG	TTG	GGG	GAC	CTC	CTG	GAC	AGT	822
147	Lys	Ala	Ser	Glu	Gln	Gly	Asp	Thr	Met	Leu	Gly	Asp	Leu	Leu	Asp	Ser	
148	165					170					175				180		
150	GAC	TGC	ACC	ACA	GGG	AGT	GGC	TCA	GGG	CTC	CCC	TTC	CTG	GTG	CAG	AGG	870
151	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	Leu	Val	Gln	Arg	
152				185					190				195				
154	ACA	GTG	GCA	CGG	CAG	GTT	GCC	TTG	GTG	GAG	TGT	GTG	GGA	AAA	GGC	CGC	918
155	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	Gly	Lys	Gly	Arg	
156			200					205					210				
158	TAT	GGC	GAA	GTG	TGG	CGG	GGC	TTG	TGG	CAC	GGT	GAG	AGT	GTG	GCC	GTC	966
159	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Leu	Trp	His	Gly	Glu	Ser	Val	Ala	Val	
160		215					220					225					
162	AAG	ATC	TTC	TCC	TCG	AGG	GAT	GAA	CAG	TCC	TGG	TTC	CGG	GAG	ACT	GAG	1014
163	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe	Arg	Glu	Thr	Glu	
164		230				235					240						
166	ATC	TAT	AAC	ACA	GTA	TTG	CTC	AGA	CAC	GAC	AAC	ATC	CTA	GGC	TTC	ATC	1062
167	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn	Ile	Leu	Gly	Phe	Ile	
168	245					250					255				260		
170	GCC	TCA	GAC	ATG	ACC	TCC	CGC	AAC	TCG	AGC	ACG	CAG	CTG	TGG	CTC	ATC	1110
171	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser	Thr	Gln	Leu	Trp	Leu	Ile	
172			265						270				275				
174	ACG	CAC	TAC	CAC	GAG	CAC	GGC	TCC	CTC	TAC	GAC	TTT	CTG	CAG	AGA	CAG	1158
175	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu	Tyr	Asp	Phe	Leu	Gln	Arg	Gln	
176			280				285				290						
178	ACG	CTG	GAG	CCC	CAT	CTG	GCT	CTG	AGG	CTA	GCT	GTG	TCC	GCG	GCA	TGC	1206
179	Thr	Leu	Glu	Pro	His	Leu	Ala	Leu	Arg	Leu	Ala	Val	Ser	Ala	Ala	Cys	
180		295				300					305						
182	GGC	CTG	GCG	CAC	CTG	CAC	GTG	GAG	ATC	TTC	GGT	ACA	CAG	GGC	AAA	CCA	1254
183	Gly	Leu	Ala	His	Leu	His	Val	Glu	Ile	Phe	Gly	Thr	Gln	Gly	Lys	Pro	
184		310				315					320						
186	GCC	ATT	GCC	CAC	CGC	GAC	TTC	AAG	AGC	CGC	AAT	GTG	CTG	GTC	AAG	AGC	1302
187	Ala	Ile	Ala	His	Arg	Asp	Phe	Lys	Ser	Arg	Asn	Val	Leu	Val	Lys	Ser	
188	325				330					335			340				
190	AAC	CTG	CAG	TGT	TGC	ATC	GCC	GAC	CTG	GGC	CTG	GCT	GTG	ATG	CAC	TCA	1350
191	Asn	Leu	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	Met	His	Ser	
192			345						350				355				
194	CAG	GGC	AGC	GAT	TAC	CTG	GAC	ATC	GGC	AAC	AAC	CCG	AGA	GTG	GGC	ACC	1398
195	Gln	Gly	Ser	Asp	Tyr	Leu	Asp	Ile	Gly	Asn	Asn	Pro	Arg	Val	Gly	Thr	
196		360				365					370						
198	AAG	CGG	TAC	ATG	GCA	CCC	GAG	GTG	CTG	GAC	GAG	CAG	ATC	CGC	ACG	GAC	1446
199	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	Gln	Ile	Arg	Thr	Asp	

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200          375          380          385
202 TGC TTT GAG TCC TAC AAG TGG ACT GAC ATC TGG GCC TTT GGC CTG GTG      1494
203 Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val
204          390          395          400
206 CTG TGG GAG ATT GCC CGC CGG ACC ATC GTG AAT GGC ATC GTG GAG GAC      1542
207 Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp
208 405          410          415          420
210 TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC CCC AGC TTT GAG      1590
211 Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu
212          425          430          435
214 GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC CCC ACC ATC CCT      1638
215 Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro
216          440          445          450
218 AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG      1686
219 Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met
220          455          460          465
222 CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG      1734
223 Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg
224          470          475          480
226 ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA      1782
227 Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys
228 485          490          495          500
230 GTG ATT CAA TAGCCCAGGA GCACCTGATT CCTTTCTGCC TGCAGGGGGC      1831
231 Val Ile Gln
233 TGGGGGGGTG GGGGGCAGTG GATGGTGCCC TATCTGGGTA GAGGTAGTGT GAGTGTGGTG      1891
235 TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTCGGCCCC CAGCCCACCC AGCCAAAAAT      1951
237 ACAGCTGGGC TGAAACCTGA AAAAAAAAAA AAA      1984
241 (2) INFORMATION FOR SEQ ID NO: 2:
242 (i) SEQUENCE CHARACTERISTICS:
243 (A) LENGTH: 503 amino acids
244 (B) TYPE: amino acid
245 (D) TOPOLOGY: linear
246 (ii) MOLECULE TYPE: protein
247 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
249 Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala
250 1          5          10          15
252 Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val
253          20          25          30
255 Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly
256          35          40          45
258 Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln
259          50          55          60
261 Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg
262 65          70          75          80
264 Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn
265          85          90          95
267 His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln
268          100          105          110
270 Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala

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```

271          115          120          125
273 Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg
274          130          135          140
276 Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser
277 145          150          155          160
279 Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp
280          165          170          175
282 Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe
283          180          185          190
285 Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val
286          195          200          205
288 Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu
289          210          215          220
291 Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe
292 225          230          235          240
294 Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile
295          245          250          255
297 Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln
298          260          265          270
300 Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe
301          275          280          285
303 Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val
304          290          295          300
306 Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr
307 305          310          315          320
309 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val
310          325          330          335
312 Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala
313          340          345          350
315 Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro
316          355          360          365
318 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln
319          370          375          380
321 Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala
322 385          390          395          400
324 Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
325          405          410          415
327 Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
328          420          425          430
330 Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
331          435          440          445
333 Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
334          450          455          460
336 Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
337 465          470          475          480
339 Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro
340          485          490          495
342 Glu Lys Pro Lys Val Ile Gln
343          500

```

## VERIFICATION SUMMARY

DATE: 01/16/2002

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TIME: 15:53:54

Input Set : N:\Crf3\RULE60\09903068.raw

Output Set: N:\CRF3\01162002\I903068.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:2726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26